Institute for Systems Genomics Networking and Tech Expo

UConn Health Center
Grossman Auditorium
Farmington, Connecticut

Monday, May 13, 2019

9:00 Registration

9:30 Welcome/Introductory Remarks
Rachel O'Neill, ISG Director, University of Connecticut

9:40 Center for Genome Innovation
Bo Reese, Ph.D., University of Connecticut

10:00 Computational Biology Core
Jill Wegryzn, Ph.D., University of Connecticut

10:20 Single Cell Genomics Center
Paul Robson, Ph.D., The Jackson Laboratory for Genomic Medicine

10:40 Microbial Analysis, Resources, and Services
Kendra Maas, Ph.D., University of Connecticut

11:00 Proteomics & Metabolomics Facility
Jeremy Balsbaugh, Ph.D., University of Connecticut

11:20 Lunch

12:15 Overview and Applications of BioRad Droplet Digital PCR, *optional*
(Grossman Auditorium)

12:30 HPC Server Tour, *optional*

1:00 **Session 1 (choose one)**
llumina Office Hours/Introduction (Demo Room)
HPC Introduction (Grossman Auditorium)

2:00 **Session 2 (choose one)**
Oxford Nanopore (Grossman Auditorium)
IPA Tutorial (Demo Room)

Center for Genome Innovation (CGI) — cgi.uconn.edu

The CGI offers a variety of training opportunities as well as NextGen sequencing and genotyping services. These services are available to UConn-affiliated researchers across all campuses and range from single run instrument access through full-service NextGen library preparation and sequencing.

The CGI also offers laboratory-based workshops for NextGen sequencing, genotyping, workflows and data analysis.

Computational Biology Core (CBC) — bioinformatics.uconn.edu

The CBC provides computational power and technical support to both academia and industry. These services are available to faculty and students within the University system. Services provided: research collaboration; project design and data analysis consultation; bioinformatics support for NextGen sequencing; software development; and access to computational resources.

Upcoming Events: Visit a complete list at https://bioinformatics.uconn.edu/cbc-workshops/

Workshop: RNA-Seq model systems
Date: May 30-31, 2019
Time: 9.00 am - 5.00 pm
Location: UCHC
Cost: $500

Workshop: Single-cell genomics
Date: July 25-26, 2019
Time: 9.00 am - 5.00 pm
Location: UCHC
Cost: $500

Workshop: Variant Detection
Date: August 22-23, 2019
Time: 9.00 am - 5.00 pm
Location: ESB - Storrs
Cost: $500

Single Cell Genomics Center — core.uconn.edu/resources/JAX

The Jackson Laboratory Single Cell Biology Laboratory develops and offers single cell capabilities to UConn investigators. The Single Cell Genomics Center works closely with the JAX-GM Flow Cytometry and JAX-GM Genome Technologies in implementing single cell workflows from tissue sample to sequence and assists in the implementation of single cell-specific bioinformatics workflows with JAX-GM Computational Sciences.

Microbial Analysis, Resources, and Services (MARS) — mars.uconn.edu

The Microbial Analysis, Resources and Services (MARS) facility supports research specializing in the analysis of microbial samples and high-throughput processing of nucleic acids. Examples include the characterization of microbiomes, sequencing of small genomes, 96-well and 384-well PCR setup or DNA quantification and other automated liquid handling applications. Services are available a la carte, ranging from fee-for-service to unassisted use of the equipment by trained and certified users.

Proteomics & Metabolomics Facility — proteomics.uconn.edu

The Proteomics & Metabolomics Facility implements ultra-high performance liquid chromatography (UPLC) coupled to high resolution mass spectrometry (MS) to unambiguously identify proteins, peptides and small molecules in complex biological mixtures. The full-service proteomics platform includes targeted (Parallel Reaction Monitoring) and untargeted quantification and identification of proteins and post-translational modifications using label-free or label-based methods. The user-operated metabolomics platform includes UPLC-MS instrument training for users interested in hands-on analytical experience in untargeted metabolite analysis.